Amendments to the Specification

PAGE 7

At line 1, before "The present invention …, please insert:

--"BRIEF DESCRIPTION OF THE DRAWINGS"--

Please replace the paragraphs at lines 3-13 with the following:

Fig. 1 represents a standard curve for an mtDNA sequence **I'** (~~circles~~diamonds) plus data for nucleotide sequence I (squares);

Fig. 2 represents a standard curve for a nuclear DNA sequence II' (~~circles~~diamonds) plus data for nucleotide sequence II (squares);

Fig. 3 represents a standard curve for a nuclear DNA sequence II (~~circles~~diamonds) plus data for nucleotide sequence I (squares);

Fig. 4 represents a standard curve for a nuclear DNA sequence II' (FasL) (~~circles~~diamonds) plus data for nucleotide sequence II (squares); and

At line 35, please delete

"http://www.ncbi.nlm.nih.gov/blast/"

and insert therefor:

--Worldwide web URL: ncbi.nlm.nih.gov/blast/--

PAGE 8

Please replace the two paragraphs from lines 5-16 with the following paragraphs.

To monitor the progress of amplification, a probe was used for nucleotide sequence I, the probe having a length of 23 nucleotides, having a FAM (carboxy fluorescein) fluorescent probe at the 5' end and a BLACKHOLE QUENCHER 1™ ~~BlackHole Quencher1™~~ group at the 3' end. This probe, and all others in this application, 10 was ordered commercially with MWG, Ebersberg, Germany. The sequence of the probe was checked to be unique for human mtDNA using Blast software, through the NCBI site as mentioned above.

The probe used for nucleotide II had a length of 22 nucleotides and contained TEXAS RED™ ~~TexasRed~~ as the fluorescent label and a BLACKHOLE QUENCHER2™ ~~BlackHole Quencher2™~~ group at the 3' end (MWG).

Please replace the paragraph beginning at line 31 and continuing through page 9, line 8, with the following paragraph:

Amplification

Amplification was performed using an iCycler® Thermal cycler (BioRad, Hercules, CA, USA) using standard procedures. The amplification is performed in plates having 96 wells. This instrument allows monitoring of fluoresence in up to 4 different channels. In short, one cycle of denaturation (95°C for 6 min) was performed, followed by 45 cycles of amplification (94°C for 30 s, 60°C for 60 s). The amplification was performed in a mix that consisted of: Promega PCR buffer 1X (Promega, Madison, WI, USA), 3.0 mM $MgC1_2$, 400 pmol of primers for mtDNA, 0.2 nM dNTP and 2 U of *Taq* polymerase (Promega). In accordance with the invention, the amplification for both nucleotide sequences I and II were performed in a single well, and the same is true for nucleotide sequences I' and II' (for determining the standard curves). Data were analysed using the software of the iCycler®.